

Schmitzer

CRF Errors Corrected by the STIC System Branch

1632

Serial Number: 08/973,363

CRF Processing Date: 11/18/2000  
Edited by: JW  
V rified by: JW (STIC staff)

- Changed a file from non-ASCII to ASCII
- Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- Edited a format error in the Current Application Data section, specifically: ENTERED
- Edited the Current Application Data section with the actual current number. The number inputted by the applicant was  the prior application data; or  other \_\_\_\_\_.
- Added the mandatory heading and subheadings for "Current Application Data".
- Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- Deleted:  non-ASCII "garbage" at the beginning/end of files;  secretary initials/filename at end of file;  page numbers throughout text;  other invalid text, such as \_\_\_\_\_
- Inserted mandatory headings, specifically: \_\_\_\_\_
- Corrected an obvious error in the response, specifically: \_\_\_\_\_
- Edited identifiers where upper case is used but lower case is required, or vice versa.
- Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- Other: Moved (iv) CORRECTION, ADDRESS: section up a few lines

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

**RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/973,363**

DATE: 01/18/2000  
TIME: 14:03:25

**INPUT SET: S34486.raw**

**This Raw Listing contains the General Information Section and up to the first 5 pages.**

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/973,363DATE: 01/18/2000  
TIME: 14:03:25

INPUT SET: S34486.raw

47 (C) TELEX:  
 48 (2) INFORMATION FOR SEQ ID NO: 1:  
 49 (i) SEQUENCE CHARACTERISTICS:  
 50 (A) LENGTH: 723 base pairs  
 51 (B) TYPE: nucleic acid  
 52 (C) STRANDEDNESS: double  
 53 (D) TOPOLOGY: linear  
 54 (ii) MOLECULE TYPE: DNA (genomic)  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 56 CCCGGTCGGA GGTTTCAAGG AATGACTAGA TGTGGCACTT AGTGCATGG TCTAGTTGAC 60  
 57 AAGGTGATGG TTGGTCAAAA GTTGGACTCG ATGATCTCAG AGTTTTTTTC CAGCCTTAAT 120  
 58 AATTCTATGA ATTCTGTAAT TTTATTCTTG ATCTTTTGA GCGAAGTTTG TTTGGGGATT 180  
 59 TTAGTTGGT TTCCCTGTCA CTGTTTTCTT TCCTTGAAAC TGACTTTCAT TTGCAACATG 240  
 60 AGAATTGCTG TATTGTCAG GTTACAAGTA GTGCAATGGC TGCTTAGAAG TAGTGAGAAA 300  
 61 CATTAGGGA AATACTGGAG TGAAGCAAC ACAGTGGTAC TGCCAAACTG TAGCTTTGGG 360  
 62 ATTTGAGGAG CCACAGAGTT GTATATAAAT TTGTTTAATG ATATCCTGCC CCTGCCTTCC 420  
 63 ATTAATTGCT TGTTTATGA AACCACTCTT TTTTTTTTTT GGCTTCTTCA 480  
 64 TATCCTGTGG TAATGAGTTA ATGCATTTAG AAGCACATGG CAGAACTAGG AGATCTGTGG 540  
 65 ATGACAGTGG TACAGGAGCT CTGAATTTTT TAGATAAACT ATGAGAGTGG AAACAGAAAAT 600  
 66 CTGAGGCTAG TTTCTTGAGC TGACTGTAAA TTTTGAGA ATATTTCAA GACTACATTA 660  
 67 GTTGTGTGTT TGAGGAAAAA TAAAATGTTT AAGTTGTCCA TTCTTGAAA CCTCCCGACC 720  
 68 GGG 723  
 69  
 70 (2) INFORMATION FOR SEQ ID NO: 2:  
 71 (i) SEQUENCE CHARACTERISTICS:  
 72 (A) LENGTH: 153 base pairs  
 73 (B) TYPE: nucleic acid  
 74 (C) STRANDEDNESS: double  
 75 (D) TOPOLOGY: linear  
 76 (ii) MOLECULE TYPE: cDNA  
 77  
 78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 79 ATTCTTCAG ATGATCCTGA TAAAAAAACCA CAAGAAAAC AGTTACAGAC CAAAAAAACCA 60  
 80 CAAGCAAAC AGTTACAGAC CCGTGCAGAC TACCTCATCA AACTACTTAG CAGAGATCTT 120  
 81 GCAAAAGAG AGGCTCAGAG ACTTTGTGGT GCG 153  
 82  
 83 (2) INFORMATION FOR SEQ ID NO: 3:  
 84 (i) SEQUENCE CHARACTERISTICS:  
 85 (A) LENGTH: 153 base pairs  
 86 (B) TYPE: nucleic acid  
 87 (C) STRANDEDNESS: double  
 88 (D) TOPOLOGY: linear  
 89 (ii) MOLECULE TYPE: cDNA  
 90 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 91 ATTTTACCTG ATGATCCAGA CAAGAAAACC CAGGCAAAGC AGCTACAGAC CAAGAAAACC 60  
 92 CAGGCAAAGC AGCTACAGAC CCGTGCAGAC TACCTCATTA AATTACTGAA TAAAGACCTT 120  
 93 GCAAGAAAAG AAGCACAAAG GCTTGCTGGT GCA 153  
 94 (2) INFORMATION FOR SEQ ID NO: 4:  
 95  
 96 (i) SEQUENCE CHARACTERISTICS:  
 97 (A) LENGTH: 153 base pairs  
 98 (B) TYPE: nucleic acid  
 99 (C) STRANDEDNESS: double

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PATENT APPLICATION US/08/973,363DATE: 01/18/2000  
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100 (D) TOPOLOGY: linear  
101 (ii) MOLECULE TYPE: cDNA  
102 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
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104 ATTTTACCTG ATGATCCAGA TAAGAAACCC CAGGCTAACGC AGTTACAGAC CAAGAAACCC 60  
105 CAGGCTAACGC AGTTACAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT 120  
106 GCAAGAAAAG AAGCACAGAG ACTTGCTGGT GCA 153  
107  
108 (2) INFORMATION FOR SEQ ID NO: 5:  
109 (i) SEQUENCE CHARACTERISTICS:  
110 (A) LENGTH: 153 base pairs  
111 (B) TYPE: nucleic acid  
112 (C) STRANDEDNESS: double  
113 (D) TOPOLOGY: linear  
114 (ii) MOLECULE TYPE: cDNA  
115 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
116 ATTTTACCTG ATGACCCAGA TAAGAAACCA CAGGCAAAGC AGTTGCAGAC CAAGAAACCA 60  
117 CAGGCAAAGC AGTTGCAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT 120  
118 GCAAGAAAAG AAGTCAAAG ACTTACTGGT GCA 153  
119  
120 (2) INFORMATION FOR SEQ ID NO: 6:  
121 (i) SEQUENCE CHARACTERISTICS:  
122 (A) LENGTH: 41 amino acids  
123 (B) TYPE: amino acid  
124 (C) STRANDEDNESS:  
125 (D) TOPOLOGY: linear  
126 (ii) MOLECULE TYPE: peptide  
127 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
128 Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln 15  
129 1 5 10 15  
130 Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Ser Arg Asp Leu Ala Lys  
131 20 25 30  
132 Arg Glu Ala Gln Arg Leu Cys Gly Ala  
133 35 40  
134  
135 (2) INFORMATION FOR SEQ ID NO: 7:  
136 (i) SEQUENCE CHARACTERISTICS:  
137 (A) LENGTH: 41 amino acids  
138 (B) TYPE: amino acid  
139 (C) STRANDEDNESS:  
140 (D) TOPOLOGY: linear  
141 (ii) MOLECULE TYPE: peptide  
142 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
143 Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln 15  
144 1 5 10 15  
145 Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg  
146 20 25 30  
147 Lys Glu Ala Gln Arg Leu Ala Gly Ala  
148 35 40  
149  
150 (2) INFORMATION FOR SEQ ID NO: 8:  
151 (i) SEQUENCE CHARACTERISTICS:  
152 (A) LENGTH: 41 amino acids

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/973,363DATE: 01/18/2000  
TIME: 14:03:26

INPUT SET: S34486.raw

153 (B) TYPE: amino acid  
 154 (C) STRANDEDNESS:  
 155 (D) TOPOLOGY: linear  
 156 (ii) MOLECULE TYPE: peptide  
 157 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
 158 Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln  
 159 1 5 10 15  
 160 Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg  
 161 20 25 30  
 162 Lys Glu Ala Gln Arg Leu Ala Gly Ala  
 163 35 40  
 164  
 165 (2) INFORMATION FOR SEQ ID NO: 9:  
 166 (i) SEQUENCE CHARACTERISTICS:  
 167 (A) LENGTH: 41 amino acids  
 168 (B) TYPE: amino acid  
 169 (C) STRANDEDNESS:  
 170 (D) TOPOLOGY: linear  
 171 (ii) MOLECULE TYPE: peptide  
 172 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
 173 Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln  
 174 1 5 10 15  
 175 Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg  
 176 20 25 30  
 177 Lys Glu Val Gln Arg Leu Thr Gly Ala  
 178 35 40  
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 180 (2) INFORMATION FOR SEQ ID NO: 10:  
 181 (i) SEQUENCE CHARACTERISTICS:  
 182 (A) LENGTH: 6608 base pairs  
 183 (B) TYPE: nucleic acid  
 184 (C) STRANDEDNESS: double  
 185 (D) TOPOLOGY: linear  
 186 (ii) MOLECULE TYPE: cDNA  
 187 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
 188 CGGGCTGGGG CACGAAGCGC ACCGCCGGGC CACCGAGGCT CGGGCCGGGG AAGGCCTGGC 60  
 189 CCGCCGAGGC GGACGCCACGC AGGTATTTGG GCAAAATCT TGGCCATCTG TAGAGAATAG 120  
 190 CAAGTCAAAC GCATTACTTC GAAAACATAC GGAGTACCAAG AAAGGGGATT CTTGACCTAC 180  
 191 ACCTTGTAAAC CTGAGTGGAC TTTCCTTTTA ACTTCTTAAT ACTTACAATG AATGGGCACA 240  
 192 GTGATGAAGA AAGTGTAAAGA AACAGCAGTG GAGAGTCAAG CAGATCAGAT GATGATTCTG 300  
 193 GGTCAAGCTTC AGGTTCTGGA TCTGGTTCAA GCTCTGGAAG CAGTAGCGAT GGAAGTAGCA 360  
 194 GCCAGTCAGG TAGCAGTGAC TCTGAATCTG GTTCAGAGTC AGGCAGTCAA TCCGAATCAG 420  
 195 AGTCTGACAC ATCTAGAGAG AAGAAACAAAG TTCAAGCTAA ACCTCCGAAA GCTGACGGAT 480  
 196 CTGAGTTTG GAAGTCCAGT CCAAGCATAAC TTGCTGTACA GAGATCAGCA GTGCTCAAGA 540  
 197 AGCAACAGCA ACAGCAAAAA GCAGCATCAT CAGACAGTGG TTCAGAAAGAG GACTCATCCA 600  
 198 GTAGTGAAGA TTCTGGCGAT GATTCTGCTCA GTGAAACTAA GAAGAAAAAG CATAAAAGATG 660  
 199 AAGACTGGCA AATGTCAGGG TCAGGGTCAG TATCAGGAAC TGGTTCTGAT TCTGAATCGG 720  
 200 CGGAAGATGG GGATAAAAGC AGTTGTGAAG AAAGTGAATC TGACTATGAG CCAAAAAACA 780  
 201 AAGTCAAAG CCGTAAACCT CCAAGCAGAA TTAAGCCAAA AAGTGGAAA AAGAGCACAG 840  
 202 GACAGAAGAA GAGGCAACTT GATTCTGCTCA AGGAGGAGGA GGACGATGAT GAAGATTATG 900  
 203 ATAAGAGAGG ATCTCGTCGC CAGGCAACAG TGAATGTTAG TTACAAAGAA GCTGAAGAAA 960  
 204 CCAAGACAGA TTCTGATGAT TTGCTGGAAG TTTGTGGAGA GGATGTCCCA CAGACTGAAG 1020  
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RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/973,363DATE: 01/18/2000  
TIME: 14:03:26

## INPUT SET: S34486.raw

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209	TCCATA	ACAC	TTGGGAA	ACT	GAAGAA	ACGC	TGAAGC	AA	ATGTT	AAA	GGAATG	AA	1260							
210	AACTGG	ACAA	CTACA	AGAAA	AAGGAT	CAGG	AGAC	AAAACG	CTGG	CTGAAA	AATG	CTTC	1320							
211	CAGAAG	ATGT	GGA	ATATT	AACT	GCCAGC	AGGAGC	TTAC	AGATG	ATCTG	CACAA	ACAT	1380							
212	ATCAA	ATAGT	GGAAA	AGATA	ATTG	GCTC	ATT	CAA	ATC	A	GTCAG	CAGCT	GGTTAT	CCGG	1440					
213	ACTACT	ATTG	CAA	ATGGC	CAG	GGT	CTGC	CTT	ACTC	AGATG	TAGCT	GGGAA	GATGG	TGCTC	1500					
214	TCATTG	CCAA	AAAG	TTTC	CAG	GCAC	GC	CATTG	ATGAGT	TATT	TAGC	CAGAA	AT	CAATCC	AA	1560				
215	CTACT	CCCTT	TAAGG	ACTG	GC	AAGG	TTCTAA	AA	CAGA	GAGACC	AAGA	TTTGTT	GC	ACTG	AA	1620				
216	AGCAAC	CATC	TTAC	ATTG	GA	GGAC	ATG	AAA	GT	CTGG	AG	TT	AAGA	GATT	T	1680				
217	GATT	GAATT	G	CTCG	C	CT	ATG	GGT	G	CA	A	AGGAA	ATAG	TTG	TATT	CTT	1740			
218	TGGGT	CTGGG	TAAA	ACA	ATA	CAA	ACA	ATT	CTT	TTCTG	AA	CTAC	CTG	TTT	CATG	AA	1800			
219	AACT	GTAT	GG	CCCT	TTCT	CTG	CG	GTG	CA	CT	TTCT	TAC	CTT	GAC	ATCT	TGGC	AAAGAG	1860		
220	AGATT	CAAC	TTGG	GCTC	C	CAGA	GTG	ATG	CTG	AGT	TTA	CTT	AGGAG	AT	A	TA	ACTAGT	1920		
221	GAA	ATAT	GAT	AAGG	ACT	CAT	GA	ATGG	ATG	TC	ATCC	ACAGAC	TA	AA	ACG	ATTA	ACA	1980		
222	TACT	CTG	AC	GAC	AT	ATG	AA	TTT	ACT	G	AGG	ATA	AGTC	AT	TC	CTT	G	2040		
223	GGGC	ATT	CAT	AGG	AGT	TG	GA	AGC	T	ATC	TG	AA	TG	ACT	CT	CT	TG	ACA	2100	
224	GG	ACT	TTAA	AG	ACT	TA	AG	TCA	AA	CC	AC	CAT	TC	TT	G	AA	CC	AC	2160	
225	AT	TC	CC	CT	CAA	AG	AG	CTG	TTG	T	CTT	TG	TG	TT	GC	AA	TT	CT	2220	
226	GGG	AA	GAT	TT	TGA	AG	AGG	GAG	CAT	GG	CAA	AG	GA	AG	AG	TT	TG	TG	2280	
227	AAG	AG	CT	TG	AC	CA	AT	TTT	TA	CTA	AGA	AG	AG	TT	AA	AGA	TG	TG	2340	
228	CTA	AGG	TTG	GA	AC	AA	ATT	CTG	AG	GG	AA	GG	TG	AG	CC	AT	CA	AG	2400	
229	GG	AT	TTT	AA	C	A	AG	AA	TT	AA	GG	TT	AG	GG	AA	GG	CT	AC	2460	
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231																				
232	CAGA	GATA	AA	TGA	ATT	CT	TA	T	A	AA	AA	CAGG	AG	GC	TT	TG	GATA	CG	2580	
233	GGAA	AA	CTA	AT	C	TT	CT	TG	AC	A	G	T	CT	GA	T	GC	GA	CAGAGT	TC	2640
234	TG	AT	TTT	CTC	T	C	AGA	T	GGT	G	GG	T	G	C	T	G	T	TAT	CGCC	2700
235	AG	TTT	CC	CC	TT	CC	AGA	G	ACT	CT	AG	AT	AT	CTG	T	AG	T	ACT	GG	2760
236	ATC	AT	TTT	CAA	TG	CAGA	AG	GA	TC	AG	AG	G	GG	AT	T	GT	CT	A	AGAGCTGGAG	2820
237	GATT	AGG	TAT	TA	ACT	GG	CA	T	CTG	G	CT	G	TG	TTT	TT	TG	ATT	TCT	GACTGGAATC	2880
238	CAC	AGA	AT	GA	TCT	GC	AGG	CG	AGG	CG	AG	AG	AG	GA	AG	AA	AC	AGGTTA	2940	
239	AT	AT	TTT	ATC	G	CTG	ATG	TCA	AA	AGG	ATC	AG	AGA	AGA	T	AT	T	CTG	AA	3000
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241	TG	CAT	AC	AG	TT	CA	AA	CTC	CA	CC	TTT	TTA	AA	AA	GA	AG	AG	T	3120	
242	TTT	TG	AA	G	TT	TG	GT	G	GA	ACT	CTT	TA	AA	GA	AC	CT	GA	GG	3180	
243	AGG	AA	AT	GG	T	AT	AG	AT	G	AA	CT	GA	AG	GG	AA	AA	GG	CT	3240	
244	CATT	GACT	GT	AG	GGG	AT	G	GG	TG	TT	TG	CA	AG	GT	TT	GG	GA	ACT	TT	3300
245	ATG	AA	GAT	GA	T	AT	TG	AG	TTG	GA	AC	CC	AG	AA	TT	GG	GA	AA	TG	3360
246	CAG	AA	AT	CCC	A	CGG	AGA	AG	TT	GA	AG	AA	AG	AG	AC	TT	GA	AA	AT	3420
247	ACAT	GCT	CC	G	AGG	AT	G	G	A	CT	GT	G	AA	GAT	CA	CT	TA	AT	GGG	3480

PAGE: 1

**RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/973,363**

DATE: 01/19/2000  
TIME: 01:34:47

### **INPUT SET: S34486.raw**

**This Raw Listing contains the General Information Section and up to the first 5 pages.**

1 SEQUENCE LISTING  
2  
3 (1) General Information:  
4 (i) APPLICANT:  
5 (A) NAME: GRIFFITHS, RICHARD  
6 (B) STREET: 20 (TR) Woodcroft Avenue, Broomhill,  
7 (C) CITY: Glasgow  
8 (D) COUNTRY: United Kingdom  
9 (F) POSTAL CODE (ZIP): G11 7HX  
10  
11 (A) NAME: TIWARI, BELA  
12 (B) STREET: 4 Upway Road  
13 (C) CITY: Oxford  
14 (D) COUNTRY: United Kingdom  
15 (F) POSTAL CODE (ZIP): OX3 9QH  
16 (ii) TITLE OF INVENTION: AVIAN GHD GENES AND THEIR USE IN METHODS FOR  
17 SEX IDENTIFICATION IN BIRDS  
18 (iii) NUMBER OF SEQUENCES: 39  
19 (iv) COMPUTER READABLE FORM:  
20 (A) MEDIUM TYPE: Floppy disk  
21 (B) COMPUTER: IBM PC compatible  
22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
24 (vi) *CURRENT APPLICATION DATA: i-add headings*  
25 (vii) *←←* PRIOR APPLICATION DATA:  
26 (A) APPLICATION NUMBER: WO PCT/GB96/01341  
27 (B) FILING DATE: 05-JUN-1996  
28 (viii) *←←* PRIOR APPLICATION DATA:  
29 (A) APPLICATION NUMBER: GB 9511439.3  
30 (B) FILING DATE: 06-JUN-1995  
31 (iv) *←←* CORRESPONDENCE ADDRESS:  
32 (A) ADDRESSEE: WENDEROTH, LIND & PONACK, L.L.P.  
33 (B) STREET: 2033 K. Street, N.W., Suite 800,  
34 (C) CITY: Washington  
35 (D) STATE: D.C.  
36 (E) COUNTRY: U.S.A.  
37 (F) ZIP: 20006  
38 (viii) ATTORNEY/AGENT INFORMATION:  
39 (A) NAME: Warren M Cheek, Jr.  
40 (B) REGISTRATION NUMBER: 33,367  
41 (C) REFERENCE/DOCKET NUMBER: 263/PPNTIR1172US  
42 (ix) TELECOMMUNICATION INFORMATION:  
43 (A) TELEPHONE: (202)-721-8200  
44 (B) TELEFAX: (202)-721-8250  
45 (C) TELEX:  
46 (2) INFORMATION FOR SEQ ID NO: 1:

**RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/973,363**

DATE: 01/19/2000  
TIME: 01:34:48

### **INPUT SET: S34486.raw**

47 (i) SEQUENCE CHARACTERISTICS:  
 48 (A) LENGTH: 723 base pairs  
 49 (B) TYPE: nucleic acid  
 50 (C) STRANDEDNESS: double  
 51 (D) TOPOLOGY: linear  
 52 (ii) MOLECULE TYPE: DNA (genomic)  
 53 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 54 CCCGGTCGGA GGTTTCAAGG AATGACTAGA TGTGGCACTT AGTGCCATGG TCTAGTTGAC 60  
 55 AAGGTGATGG TTGGTCAAAA GTTGGACTCG ATGATCTAG AGTTTTTTTC CAGCCTTAAT 120  
 56 AATCTATGA ATTCTGTAAT TTTATTCTTG ATCTTTTTGA GCGAAGTTG TTTGGGGATT 180  
 57 TTAGTTTGGT TTCCCTGTCA CTGTTTCTT TCCCTTGAAAC TGACTTTCAT TTGCAACATG 240  
 58 AGAATTGCTG TATTTGTCAG GTTACAAGTA GTGCAATGGC TGCTTAGAAG TAGTGAGAAA 300  
 59 CATTAGGGAA AATACTGGAG TGAAGCAAAC ACAGTGGTAC TGCCAAACTG TAGCTTTGGG 360  
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 61 ATTAATTGCT TGTGTTATGA AACCACTCTT TTTTTTTTTT TTTTTTTTTT GGCTTCTTCA 480  
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 63 ATGACAGTGG TACAGGAGCT CTGAATTTTT TAGATAAAACT ATGAGAGTGG AACAGAAAT 600  
 64 CTGAGGCTAG TTTCTTGAGC TGACTGTAAA TTTTGTGAGA ATATTTCAA GACTACATTA 660  
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 66 GGG  
 67  
 68 (2) INFORMATION FOR SEQ ID NO: 2:  
 69 (i) SEQUENCE CHARACTERISTICS:  
 70 (A) LENGTH: 153 base pairs  
 71 (B) TYPE: nucleic acid  
 72 (C) STRANDEDNESS: double  
 73 (D) TOPOLOGY: linear  
 74 (ii) MOLECULE TYPE: cDNA  
 75  
 76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 77 ATTCTCCAG ATGATCCTGA TAAAAAAACCA CAAGCAAAAC AGTTACAGAC CAAAAAAACCA 60  
 78 CAAGCAAAAC AGTTACAGAC CCGTGCAGAC TACCTCATCA AACTACTTAG CAGAGATCTT 120  
 79 GCAAAAGAG AGGCTCAGAG ACTTTGTGGT GCG  
 80  
 81 (2) INFORMATION FOR SEQ ID NO: 3:  
 82 (i) SEQUENCE CHARACTERISTICS:  
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 84 (B) TYPE: nucleic acid  
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 88 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 89 ATTTTACCTG ATGATCCAGA CAAGAAACCC CAGGCAAAGC AGCTACAGAC CAAGAAACCC 60  
 90 CAGGCAAAGC AGCTACAGAC CCGTGCAGAC TACCTCATTA AATTACTGAA TAAAGACCTT 120  
 91 GCAAGAAAGG AAGCACAAG GCTTGTGGT GCA  
 92 (2) INFORMATION FOR SEQ ID NO: 4:  
 93  
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PATENT APPLICATION US/08/973,363DATE: 01/19/2000  
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100 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
101  
102 ATTTTACCTG ATGATCCAGA TAAGAAACCC CAGGCTAACGC AGTTACAGAC CAAGAAACCC 60  
103 CAGGCTAACGC AGTTACAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT 120  
104 GCAAGAAAGG AACGACAGAG ACTTGCTGGT GCA 153  
105  
106 (2) INFORMATION FOR SEQ ID NO: 5:  
107 (i) SEQUENCE CHARACTERISTICS:  
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112 (ii) MOLECULE TYPE: cDNA  
113 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
114 ATTTTACCTG ATGACCCAGA TAAGAAACCA CAGGCAAAGC AGTTGCAGAC CAAGAAACCA 60  
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117  
118 (2) INFORMATION FOR SEQ ID NO: 6:  
119 (i) SEQUENCE CHARACTERISTICS:  
120 (A) LENGTH: 41 amino acids  
121 (B) TYPE: amino acid  
122 (C) STRANDEDNESS:  
123 (D) TOPOLOGY: linear  
124 (ii) MOLECULE TYPE: peptide  
125 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
126 Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln  
127 1 5 10 15  
128 Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Ser Arg Asp Leu Ala Lys  
129 20 25 30  
130 Arg Glu Ala Gln Arg Leu Cys Gly Ala  
131 35 40  
132  
133 (2) INFORMATION FOR SEQ ID NO: 7:  
134 (i) SEQUENCE CHARACTERISTICS:  
135 (A) LENGTH: 41 amino acids  
136 (B) TYPE: amino acid  
137 (C) STRANDEDNESS:  
138 (D) TOPOLOGY: linear  
139 (ii) MOLECULE TYPE: peptide  
140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
141 Ile Leu Pro Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln  
142 1 5 10 15  
143 Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg  
144 20 25 30  
145 Lys Glu Ala Gln Arg Leu Ala Gly Ala  
146 35 40  
147  
148 (2) INFORMATION FOR SEQ ID NO: 8:  
149 (i) SEQUENCE CHARACTERISTICS:  
150 (A) LENGTH: 41 amino acids  
151 (B) TYPE: amino acid  
152 (C) STRANDEDNESS:

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153 (D) TOPOLOGY: linear  
 154 (ii) MOLECULE TYPE: peptide  
 155 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
 156 Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln  
 157 1 5 10 15  
 158 Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg  
 159 20 25 30  
 160 Lys Glu Ala Gln Arg Leu Ala Gly Ala  
 161 35 40  
 162  
 163 (2) INFORMATION FOR SEQ ID NO: 9:  
 164 (i) SEQUENCE CHARACTERISTICS:  
 165 (A) LENGTH: 41 amino acids  
 166 (B) TYPE: amino acid  
 167 (C) STRANDEDNESS:  
 168 (D) TOPOLOGY: linear  
 169 (ii) MOLECULE TYPE: peptide  
 170 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
 171 Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln  
 172 1 5 10 15  
 173 Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg  
 174 20 25 30  
 175 Lys Glu Val Gln Arg Leu Thr Gly Ala  
 176 35 40  
 177  
 178 (2) INFORMATION FOR SEQ ID NO: 10:  
 179 (i) SEQUENCE CHARACTERISTICS:  
 180 (A) LENGTH: 6608 base pairs  
 181 (B) TYPE: nucleic acid  
 182 (C) STRANDEDNESS: double  
 183 (D) TOPOLOGY: linear  
 184 (ii) MOLECULE TYPE: cDNA  
 185 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
 186 CCGGGCTGCGG CACGAAGCGC ACCGCCGGCG CACGCAGGCT CGGGCCGGGG AAGGCCTGGC 60  
 187 CCGCCGAGCC GGACGCACGC AGGTATTTGG GCAAAAATCT TGGCCATCTG TAGAGAATAG 120  
 188 CAAGTCAAAC GCATTACTTC GAAAACATAC GGAGTACCAAG AAAGGGGATT CTTGACCTAC 180  
 189 ACCTTGTAAC CTGAGTGGAC TTTCTTTTA ACTTCTTAAT ACTTACAATG ATGGGCACCA 240  
 190 GTGATGAAGA AAGTGTAAAG AACAGCAGTG GAGAGTCAG CAGATCAGAT GATGATTCTG 300  
 191 GGTCACTTTC AGGTTCTGGA TCTGGTTCAA GCTCTGGAAG CAGTAGCGAT GGAAGTAGCA 360  
 192 GCCAGTCAGG TAGCAGTGAC TCTGAATCTG GTTCAGAGTC AGGCAGTCAA TCCGAATCAG 420  
 193 AGTCTGACAC ATCTAGAGAG AAGAAACAAAG TTCAAGCTAA ACCTCCGAAA GTCGACGGAT 480  
 194 CTGAGTTTTG GAAGTCAGT CCAAGCATAAC TTGCTGTACA GAGATCAGCA GTGCTCAAGA 540  
 195 AGCAACAGCA ACAGCAAAAAA GCAGCATCAT CAGACAGTGG TTCAGAAGAG GACTCATCCA 600  
 196 GTAGTGAAGA TTCTGCGCAT GATTGTCCTA GTGAAACTAA GAAGAAAAAG CATAAAAGATG 660  
 197 AAGACTGGCA AATGTCAGGG TCAGGGTCAG TATCAGGAAC TGTTCTGTAT TCTGAATCGG 720  
 198 CGGAAGATGG GGATAAAAGC AGTTGTGAAG AAAGTGAATC TGACTATGAG CAAAAAAACA 780  
 199 AAGTCAAAAG CCGTAAACCT CCAAGCAGAA TTAAGCCAAA AAGTGGGAAA AAGAGCACAG 840  
 200 GACAGAAGAA GAGGCAACTT GATTGTCATCAG AGGAGGAGGA GGACGATGAT GAAGATTATG 900  
 201 ATAAGAGAGG ATCTGTCGC CAGGCAACAG TGAATGTTAG TTACAAAGAA GCTGAAGAAA 960  
 202 CCAAGACAGA TTCTGATGAT TTGCTGGAAAG TTTGTGGAGA GGATGTCCTCA CAGACTGAAG 1020  
 203  
 204 AAGATGAATT TGAAACTATA GAGAAGTTTA TGGACAGTCG AATTGGCCGA AAAGGAGGCCA 1080  
 205 CTGGTGCCTC AACCAACATC TATGCCGTTG AGGCAGATGG TGACCCAAAT GCTGGGTTTG 1140

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207	TCCATAACAC TTGGGAAACT GAAGAACGC TGAAGCAACA AAATGTTAAA GGAATGAACA	1260
208	AACTGGACAA CTACAAGAAA AAGGATCAGG AGACAAAACG CTGGCTGAAA AATGCTTCTC	1320
209	CAGAAGATGT GGAATATTAT AACTGCCAGC AGGAGCTTAC AGATGATCTG CACAAACAAT	1380
210	ATCAAATAGT GGAAAAGATA ATTGCTCATT CAAATCAAAA GTCAGCAGCT GGTTATCCGG	1440
211	ACTACTATTG CAAATGGCAG GGTCTGCCTT ACTCAGAATG TAGCTGGAA GATGGTGCTC	1500
212	TCATTGCCAA AAAGTTTCAG GCACGCATTG ATGAGTATT TAGCAGAAAT CAATCCAAGA	1560
213	CTACTCCCTT TAAGGACTG C AAGGTTCTAA AACAGAGACC AAGATTGTT GCACTGAAGA	1620
214	AGCAACCATC TTACATTGGA GGACATGAAA GTCTGGAGTT AAGAGATTAT CAGTTAAATG	1680
215	GATTGAATTG GCTCGCTCAT TCATGGTGC AAGGAATAG TTGATTCTT GCAAGATGAAA	1740
216	TGGGTCTGGG TAAAACAATA CAAACAATT TTCTTCTGAA CTACCTGTT CATGAACATC	1800
217	AACTGTATGG CCCTTTCTT CTGCGCTGC CACTTTCTAC CTTGACATCT TGGCAAAGAG	1860
218	AGATTCAAAC TTGGGCTCCT CAGATGAATG CTGAGTTTA CTTAGGAGAT ATAACATGTA	1920
219	GAAATATGAT AAGGACTCAT GAATGGATGC ATCCACAGAC TAAACGATTA AAGTTAACAA	1980
220	TACTTCTGAC GACATATGAA ATTCTACTGA AGGATAAGTC ATTCTCTGGT GGTCTCAATT	2040
221	GGGCATTCAT AGGAGTTGAT GAAGCTCATC GTTTAAAAAA TGATGACTCT CTTCTGTACA	2100
222	GGACTTTAAT AGACTTTAAC TCCAACCATC GACTTCTGAT TACTGGAACC CCACTGCAA	2160
223	ATTCCTCAA AGAGCTGTGG TCTTTGTTGC ATTCATCATGCCAGAAAAA TTTCCTCCT	2220
224	GGGAAGATTG TGAAGAGGAG CATGGCAAAG GAAGAGAGTA TGTTATGCA AGTCTTCACA	2280
225	AAGAGCTTGA ACCATTTTA CTAAGAAGAG TTAAAAAAGA TGAGTACCTG TCTTTACCTG	2340
226	CTAAGGTTGA ACAAAATCTG AGGATGGAAA TGAGTGCATT GCAGAAGCAA TATTACAAGT	2400
227	GGATTTAAC AAGGAATTAT AAAGCCCTCA GTAAAGGTTC AAAAGGCAGT ACCTCAGGCT	2460
228	TTCTGAACAT TATGATGGAA CTTAAGAAGT GTTGTACCA TTGCTACCTC ATTAAGCCAC	2520
229		
230	CAGATGATAA TGAATTCTAT AATAAACAGG AGGCCTTACA GCATTTGATA CGTAGCAGCG	2580
231	GGAAACTAAT CCTCTTGAC AAGCTACTGA TTCTGCTGCG AGAACGTGGC AACAGAGTT	2640
232	TGATTTCTC TCAGATGGTG AGGATGCTGG ACATCCTAGC AGAATATCTG AAGTATGCC	2700
233	AGTTTCCCTT CCAGAGACTT GATGGATCAA TAAAAGGGGA ATTGAGGAAG CAAGCACTGG	2760
234	ATCATTCAA TGCAGAAGGA TCAGAGGATT TCTGTTTTT ACTGCTACA AGAGCTGGAG	2820
235	GATTAGGTAT TAACTGGCA TCTGCTGACA CTGAGTTAT TTTGATTCT GACTGGAATC	2880
236	CACAGAATGA TCTGCAGGCA CAGGGCAGAG CTCATAGAAT TGGACAGAAAG AAACAGGTTA	2940
237	ATATTTATCG GCTAGTCACA AAAGGATCAG TAGAAGAAGA TATTCTTGAA AGAGCCAAGA	3000
238	AGAAGATGGT GCTAGACCAT TTAGTAATTG AGAGAATGGA CACGACAGGA AAAACTGTT	3060
239	TGCATACAGG TTCAACTCCA TCAAGCTCTA CACCTTTAA TAAAGAAGAG TTATCAGCTA	3120
240	TTTTGAAGTT TGGTCTGAG GAACCTTTA AAGAACCTGA AGGAGAAGAA CAGGAGCCCC	3180
241	AGGAAATGGA TATAGATGAA ATCTTGAAAGA GAGCTGAAAC TCGGGAAAAT GAGCCAGGTC	3240
242	CATTGACTGT AGGGGATGAG TTGCTTTACAG AGTTCAAGGT GGGAACTTT TCCAATATGG	3300
243	ATGAAGATGA TATTGAGTTG GAACCGAAA GAAATTCAAG AAATTGGAA GAAATCATCC	3360
244	CAGAATCCC ACGGAGAAGG ATAGAGGAGG AGGAAAGACA AAAAGAACTT GAAGAAATAT	3420
245	ACATGCTCCC GAGGATGAGA AACTGTGCAA AACAGATCAG CTTTAATGGG AGTGAAGGAA	3480
246	GACGCAGTAG GAGCAGAAGA TATTCTGGAT CTGATAGTGA CTCCATCACA GAAAGAAAAC	3540
247	GGCCAAAAAA GCGTGGAGA CCTCGAACCA TTCCCTCGAGA AAATTAAAAA GGATTTAGTG	3600
248	ATGCAGAGAT CAGGGGGTTT ATCAAGAGTT ACAAGAAATT TGGTGGCCCT CTGGAAAGGT	3660
249	TAGATGCTGT AGCTAGAGAT GCTGAACCTGG TTGATAAATC TGAGACAGAC CTTAGACGTT	3720
250	TGGGTGAAC TGTACATAAT GGATGCATTA AGGCTTAAA GGACAATTCA TCTGGACAAG	3780
251	AAAGAGCAGG AGGTAGACTT GGGAAAGTTA AAGGCCAAC GTTTCGAATC TCAGGAGTGC	3840
252	AGGTGAATGC AAAACTAGTC ATCTCTCAGC AAGAAGAGCT GGCAACACTG CACAAATCCA	3900
253	TTCCCTCAGA TCCAGAAGAA AGGAAAAGAT ATGTCATCCC ATGCCACACC AAGGCTGCTC	3960
254	ACTTCGATAT AGATTGGGGT AAAGAAGATG ATTCCAATCT GTTGTAGGC ATCTATGAAT	4020
255		
256	ATGGCTATGG CAGCTGGGA ATGATAAAAAA TGGATCCAGA TCTCAGCTTA ACACAGAAGA	4080
257	TTTTACCTG A TGATCCAGAC AAGAAACCCC AGGCAAAGCA GCTACAGACC CGTGCAGACT	4140
258	ACCTCATTAA ATTACTGAAT AAAGACCTTG CAAGAAAGGA AGCACAAAGG CTTGCTGGTG	4200

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FILING DATE  
CLASSIFICATION  
CURRENT APPLICATION DATA